



A

OsMAPK5a -----MDGAPVAEFRPTMTHGGRYLLYDI FGNKEFEVTN
 OsMAPK5b -----MDGAPVAEFRPTMTHGGRYLLYDI FGNKEFEVTN
 TaWCK-1 -----MDGAPVAEFRPTMTHGGRYLLYDI FGNKEFEITTA
 NWIPK MADANMGAGGGQFPDFPSVLTHGGQYVQFDI FGNKEFEITTT
 Consensus MDGAPVAEFRPTMTHGGR LLY IFGN FE T

I
 OsMAPK5a KYQPPIMPPIGRGAYGIVCSVMNFETREMVAIKKIANAFNN
 OsMAPK5b KYQPPIMPPIGRGAYGIVCSVMNFETREMVAIKKIAN-----
 TaWCK-1 KYQPPIMPPIGRGAYGIVCSVMNFETREMVASKKIANAFDN
 NWIPK KYRPPIMPPIGRGAYGIVCSVLNTELNEMVAVKKIANAFDI
 Consensus KYQPPIMPPIGRGAYGIVCSVMNFETREMVAIKKIANAF N

II
 OsMAPK5a DMDAKRTLREIKLLRHLHDHENIIGIRDVI PPPIPOAFNDV
 OsMAPK5b DMDAKRTLREIKLLRHLHDHENIIGIRDVI PPPIPOAFNDV
 TaWCK-1 NMDAKRTLREIKLLRHLHDHENIIGIRDVI PPPIPOAFNDV
 NWIPK YMDAKRTLREIKLLRHLHDHENIIGIRDVI PPPIRREFSDV
 Consensus MDAKRTLREIKLLRHLHDHENIIGIRDVI PP IP FNDV

III **IV**
 OsMAPK5a YIATELMDTDLHHIIRSNOELSEEHCQYFLYQILRGLKYI
 OsMAPK5b YIATELMDTDLHHIIRSNOELSEEHCQYFLYQILRGLKYI
 TaWCK-1 YIATELMDTDLHHIIRSNOELSEEHCQYFLYQILRGLKYI
 NWIPK YIATELMDTDLHHIIRSNOELSEEHCQYFLYQILRGLKYI
 Consensus YIATELMDTDLHHIIRSNOELSEEHCQYFLYQILRGLKYI

V
 OsMAPK5a HSNVTHRDLPKSNLLLNANCDLKICDFGLARPSSESDMM
 OsMAPK5b HSNVTHRDLPKSNLLLNANCDLKICDFGLARPSSESDMM
 TaWCK-1 HSNVTHRDLPKSNLLLNANCDLKICDFGLARPSSESDMM
 NWIPK HSNVTHRDLPKSNLLLNANCDLKICDFGLARPSSESDMM
 Consensus HSNVTHRDLPKSNLLLNANCDLKICDFGLARPSSESDMM

VI **VII**
 OsMAPK5a TEYVVTRWYRAPELLLNSTDYSAIDVWSVGCIFMELINR
 OsMAPK5b TEYVVTRWYRAPELLLNSTDYSAIDVWSVGCIFMELINR
 TaWCK-1 TEYVVTRWYRAPELLLNSTDYSAIDVWSVGCIFMELINR
 NWIPK TEYVVTRWYRAPELLLNSTDYSAIDVWSVGCIFMELINR
 Consensus TEYVVTRWYRAPELLLNSTDYSAIDVWSVGCIFMELINR

VIII **IX**
 OsMAPK5a OPLFPGRDHMHQMRLITEVIGTPTDDLGFI RNEDARKYM
 OsMAPK5b OPLFPGRDHMHQMRLITEVIGTPTDDLGFI RNEDARKYM
 TaWCK-1 OPLFPGRDHMHQMRLITEVIGTPTDDLGFI RNEDARKYM
 NWIPK KPLFGGKDHVHQRLLTELIGTPTADLGFI RNEDARKYM
 Consensus PLFPGRDHMHQMRLITEVIGTPTDD LGFI RNEDARKYM

X
 OsMAPK5a RHLPOYPRRTFASMFPRVQPAALDLIERMLTENPLQRTIV
 OsMAPK5b RHLPOYPRRTFASMFPRVQPAALDLIERMLTENPLQRTIV
 TaWCK-1 RHLPOYPRRTFASMFPRVQPAALDLIERMLTENPLQRTIV
 NWIPK ROLPOHPRQOLAEVFPVHNPLATDLVDKMLTFDPTRRTIV
 Consensus RHLPO PRRTFAS FP VQPAALDLIERMLTENPLQRTIV

XI
 OsMAPK5a EEALDHPYLERLHDIADPEICLPFSFDFFEOKALNE DQMK
 OsMAPK5b EEALDHPYLERLHDIADPEICLPFSFDFFEOKALNE DQMK
 TaWCK-1 EEALDHPYLERLHDIADPEICLPFSFDFFEOKALNE DQMK
 NWIPK EEALDHPYLAKLHDAGDEPICVPFSFDFFEOKGIGE E QIK
 Consensus EEALDHPYLERLHD ADEPIC PFSFDFEQ L EDQMK

OsMAPK5a QLIENEAIEMNPNI RY
 OsMAPK5b QLIENEAIEMNPNI RY
 TaWCK-1 QLIENEAIEMNPNI RY
 NWIPK DMIYQEA LSLNPEYA-
 Consensus QLIENEA E NPN RY

B

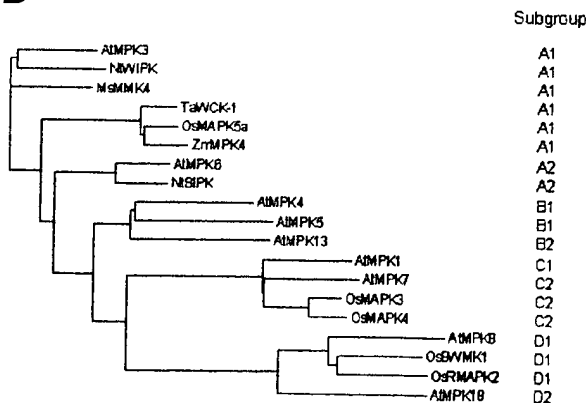


FIGURE 1

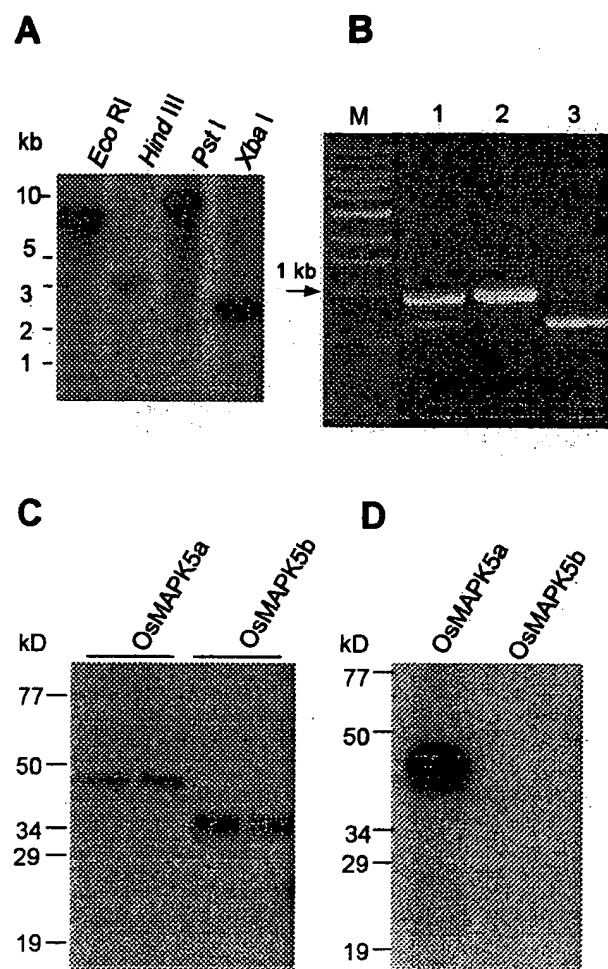


FIGURE 2

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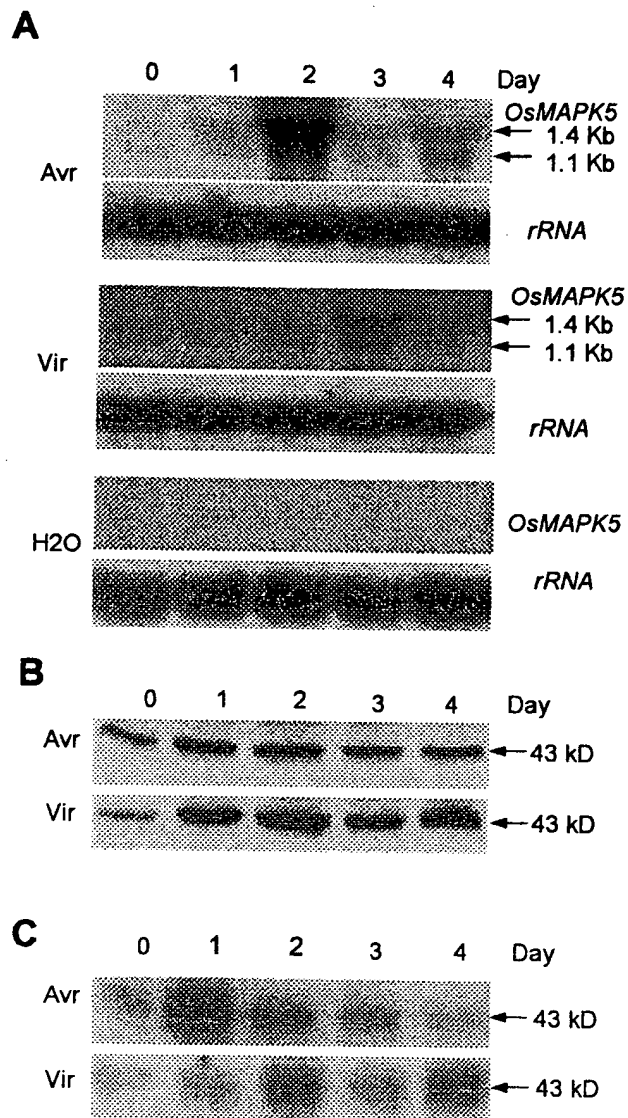


FIGURE 3

BEST AVAILABLE COPY

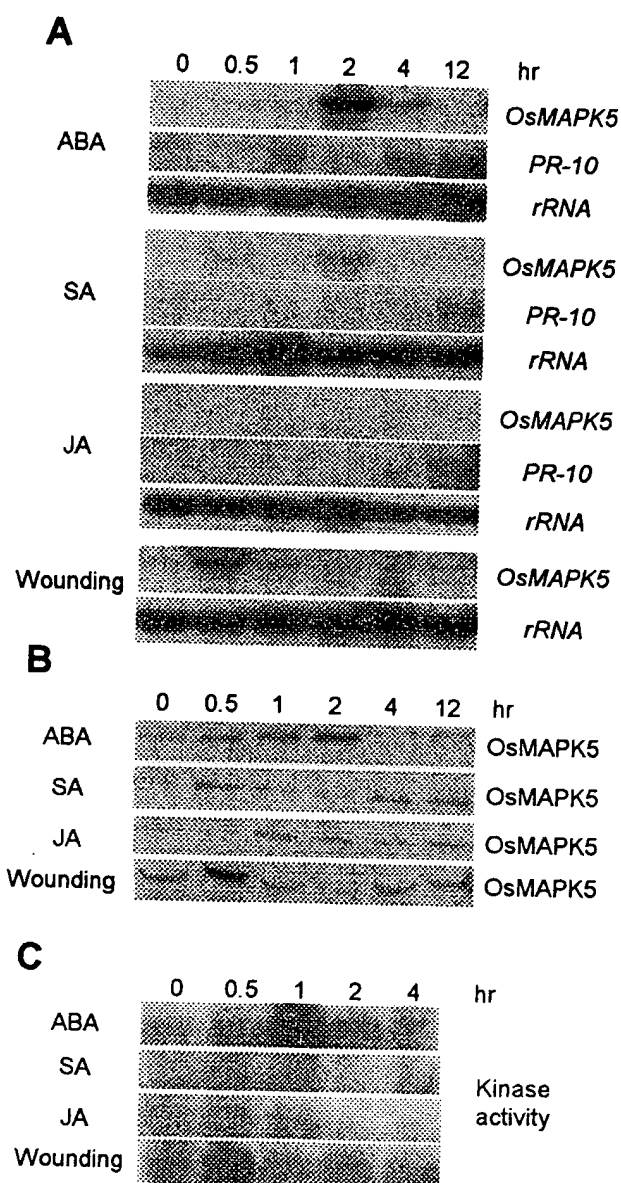
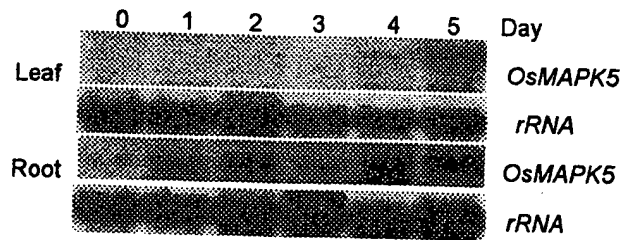


FIGURE 4

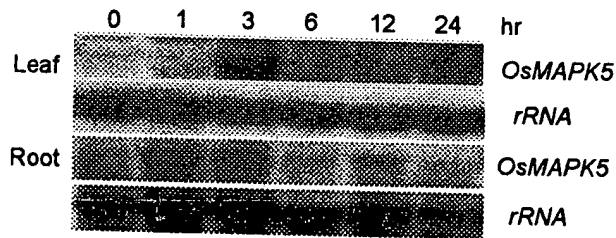
BEST AVAILABLE COPY

A

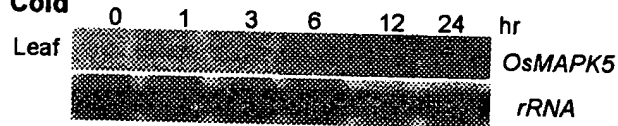
Drought



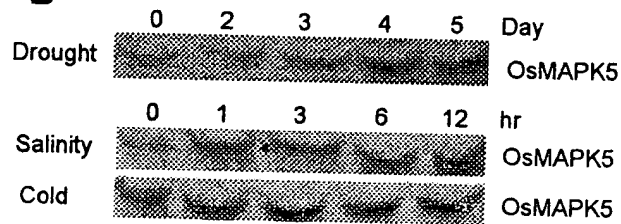
Salinity



Cold



B



C

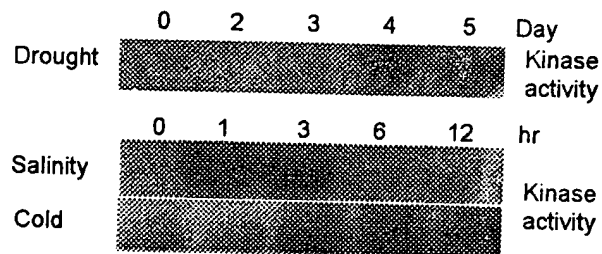


FIGURE 5

BEST AVAILABLE COPY

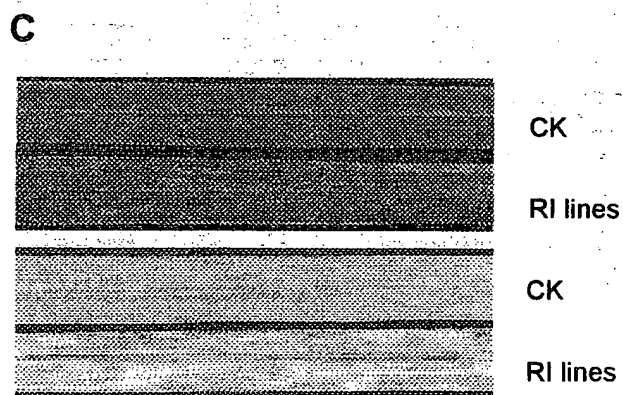
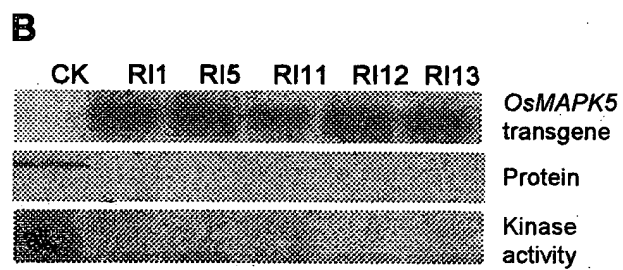
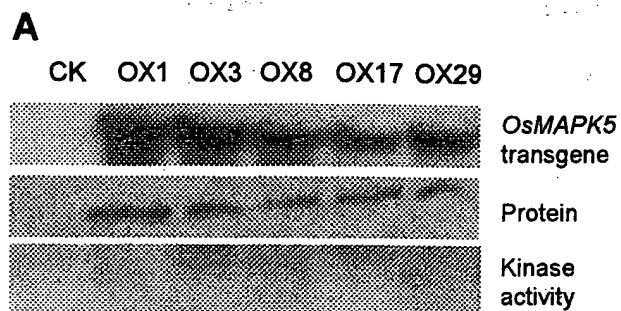
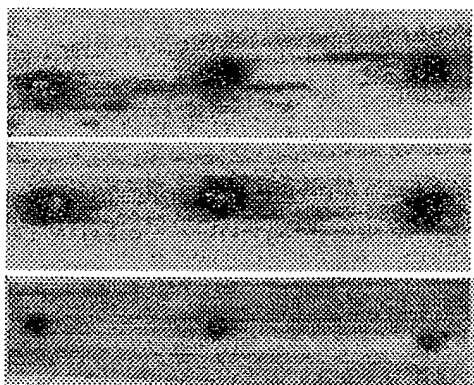


FIGURE 6

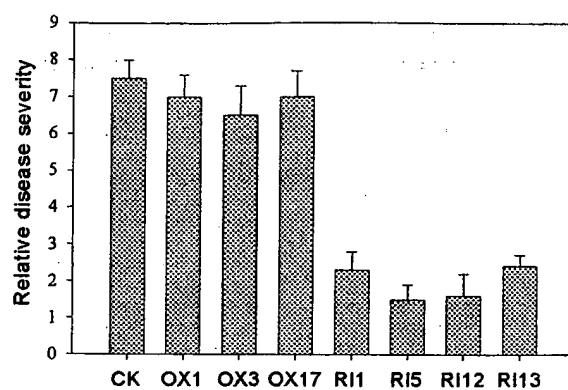
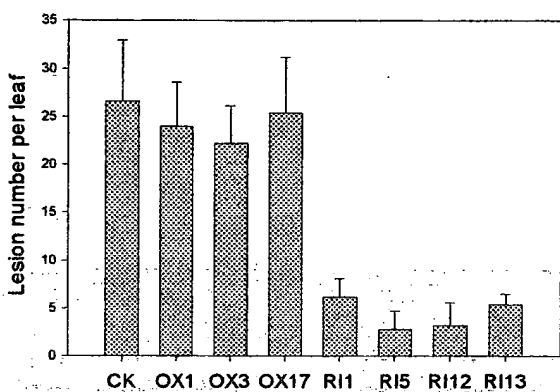
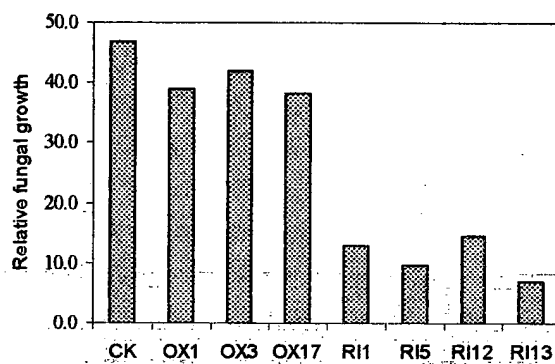
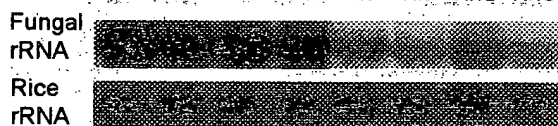
BEST AVAILABLE COPY

A

CK

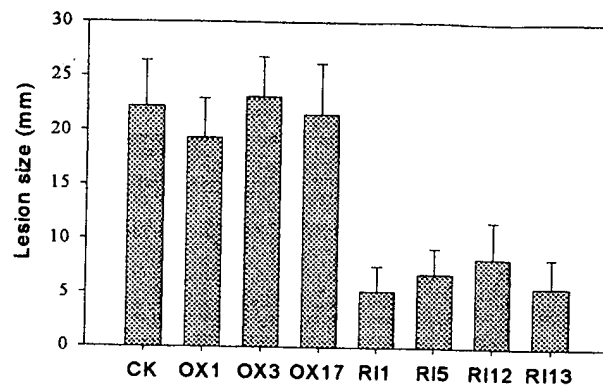
OX

RI

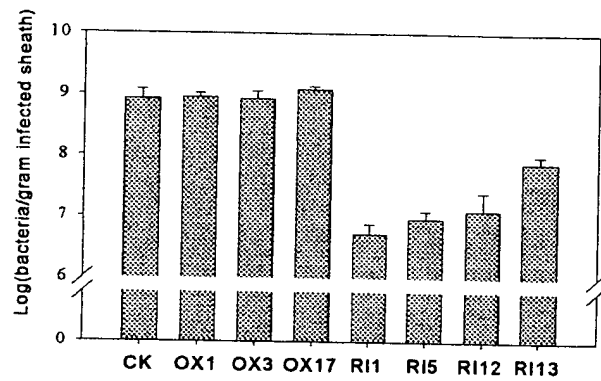
B**C****D****E****FIGURE 7**

BEST AVAILABLE COPY

A



B



C



FIGURE 8

BEST AVAILABLE COPY

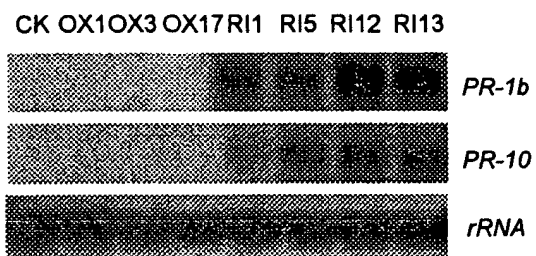
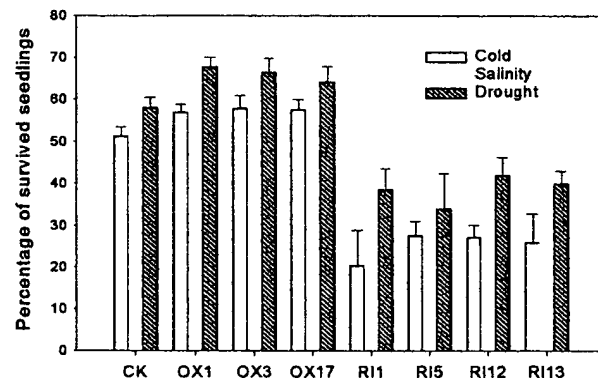


FIGURE 9

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A



B

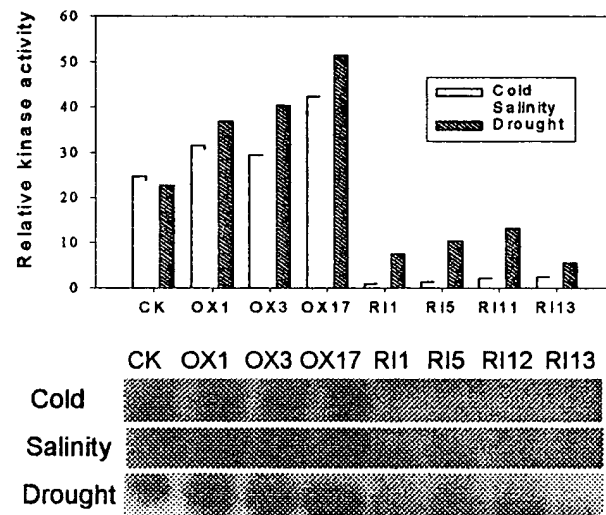


FIGURE 10

BEST AVAILABLE COPY

OsMAPK5a
SEQ. ID. NO: 1

```

1      agagagtcag ataaggtcgt taattaggtt ggtcaattcg gctgcttgcg gcgagagaag
61     aggaggaggg attagggatg gacggggcgc cggtggcgga gttcaggccg acgatgacgc
121    acggcggccg gtacctgctc tacgacatct tcgggaacaa gttcgagggtg acgaacaagt
181    accagccgcc catcatgccc attggccgcg gcgcctacgg gatcgtctgc tccgtgatga
241    actttgagac gagggagatg gtggcgataa agaagatcgc caacgcgttc aacaacgaca
301    tggacgccaa gcgcacgctc cgggagatca agctcctcag gcacctcgac caccgagaaca
361    tcataggcat cagggatgtg atcccgcgcg cgatccctca ggcggtcaac gacgtctaca
421    tcgccacgga gctcatggac accgacctcc atcacatcat ccgctccaac caagaactgt
481    cagaagagca ctgccagtat ttctgttacc agatcctgcg ggggctcaag tacatccact
541    cggcgaacgt gatccaccgc gacctgaagc cgagcaacct gctgctgaac gccaaactgcg
601    acctcaagat ctgcgacttc gggctggcgc ggccgtcgtc ggagagcgac atgatgacgg
661    agtacgtggg caccgcgtgg tacgcgcgcg cggagctgct gctcaactcc accgactact
721    ccgccgccat cgacgtctgg tccgtcggct gcatcttcat ggagctcatc aaccgccagc
781    cgctcttccc cggcagggac cacatgcacc agatgcgcct catcaccgag gtgatcggga
841    cgccgacgga cgacgagctg gggttcatac ggaacgagga cgcgaggaag tacatgaggc
901    acctgccgca gtacccgcgc cggacgttcg cgagcatgtt cccgcgggtg cagcccgcg
961    cgctcgacct catcgagagg atgctcacct tcaaccgcgt gcagagaatc acagttgagg
1021   aggcgctcga tcattccttac ctagagagat tgcacgacat cgccgatgag cccatctgcc
1081   tggagccctt ctcttcgac ttcgagcaga aggtctctaaa cgaggaccaa atgaagcagc
1141   tgatcttcaa cgaagcgatc gagatgaacc caaacatccg gtactagatt gaatcaccat
1201   ggaaatgaga tcccgtctat acctgctttg tacatatgat caagattgag agccgggtag
1261   actgaacatt gcatttgttt gtttgttgat gttcgaaacc cacattctct gcaagttgtg
1321   gctgctttgt atgatatatg gtactatggt cgaataaaaag ggtttggaac tttggattaa
1381   aaaaaaaaaa aaaaaa

```

FIGURE 11

BEST AVAILABLE COPY

OsMAPK5a
SEQ. ID. NO: 2

MDGAPVAEFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGR
GAYGIVCSVMNFETREMVAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVI
PPPIPQAFNDVYIATELMDTDLHHIIRSNQELSEHCQYFLYQILRGLKYIHSANVIH
RDLKPSNLLLNNANCDLKICDFGLARPSSESMMTEYVVTRWYRAPELLLNSTDYSAAI
DVWSVGCI FMELINRQPLEPGRDHMHQMLITEVIGTPTDDELGFIRNEDARKYMRHL
PQYPRRTFASMFPRVQPAALDLIERMLTFNPLQRITVEEALDHPYLERLHDIADEPIC
LEPFSFDFEQKALNEDQMKQLIFNEAIEMNPNI RY

FIGURE 12

OsMAPK5b
SEQ. ID. NO: 3

```

1      agagagtcag ataaggtcgt taattaggtt ggtcaattcg gctgcttgcg gcgagagaag
61     aggaggaggg attagggatg gacggggcgc cgggtggcggg gttcaggccg acgatgacgc
121    acggcggccg gtacctgctc tacgacatct tcgggaacaa gttcgagggtg acgaacaagt
181    accagccgcc catcatgccc attggccgcg gcgcctacgg gatcgtctgc tccgtgatga
241    actttgagac gagggagatg gtggcgataa agaagatcgc caactgcgac ctcaagatct
301    gcgacttcgg gctggcgccg ccgtcgtcgg agagcgacat gatgacggag tacgtgggtca
361    cccggtggta ccgcgcgcgg gagctgctgc tcaactccac cgactactcc gccgccatcg
421    acgtctggtc cgtcggctgc atcttcattg agctcatcaa ccgccagccg ctcttccccg
481    gcagggacca catgcaccag atgcgcctca tcaccgaggt gatcggggac ccgacggacg
541    acgagctggg gttcatacgg aacgaggacg cgaggaagta catgaggcac ctgccgcagt
601    acccgcgccg gacgttcgcg agcatgttcc cgcgggtgca gcccgccgcg ctcgacctca
661    tcgagaggat gctcaccttc aaccgcgtgc agagaatcac agttgaggag gcgctcgatc
721    atccttacct agagagattg cacgacatcg ccgatgagcc catctgcctg gagcccttct
781    ccttcgactt cgagcagaag gctctaaacg aggaccaa atgaagcagctg atcttcaacg
841    aagcgatcga gatgaaccca aacatccggt actagattga atcaccatgg aaatgagatc
901    ccgtctatac ctgctttgta catatgatca agattgagag ccgggtagac tgaacattgc
961    atttgtttgt ttgttgatgt tcgaaaccca cattctctgc aagttgtggc tgctttgtat
1021   gatatatggt actatgttcg aataaaaggg tttggaactt tggattaaaa aaaaaaaaaa
1081   aaaa

```

FIGURE 13

OsMAPK5b

SEQ. ID. NO: 4

MMDGAPVAEFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGR
GAYGIVCSVMNFETREMVAIKKIANCDLKICDFGLARPSSSDMMTEYVTRWYRAPE
LLNSTDYSAAIDVWSVGCI FMELINRQPLFPGRDHMHQMRLLITEVIGTPTDDELGFI
RNEDARKYMRHLPQYPRRTFASMFPVRVQPAALDLIERMLTFNPLQRITVEEALDHPYL
ERLHDIADepICLePFSFDfEQKALNEDQMKQLIFNEAIEMNPNIrY

FIGURE 14